

0590
1601

OICE

RAW SEQUENCE LISTING

DATE: 10/03/2002

PATENT APPLICATION: US/09/625,573

TIME: 14:00:12

Input Set : N:\Crif3\RULE60\09625573.raw

Output Set: N:\CRF4\10032002\I625573.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

4 (i) APPLICANT: Charo, Israel

5 Coughlin, Shaun

7 (ii) TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT

8 PROTEIN RECEPTORS

10 (iii) NUMBER OF SEQUENCES: 14

12 (iv) CORRESPONDENCE ADDRESS:

13 (A) ADDRESSEE: Cooley Godward Castro Huddleson & Tatum

14 (B) STREET: 5 Palo Alto Square

15 (C) CITY: Palo Alto

16 (D) STATE: California

17 (E) COUNTRY: USA

18 (F) ZIP: 94306-2155

20 (v) COMPUTER READABLE FORM:

21 (A) MEDIUM TYPE: Floppy disk

22 (B) COMPUTER: IBM PC compatible

23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

24 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

26 (vi) CURRENT APPLICATION DATA:

C--> 27 (A) APPLICATION NUMBER: US/09/625,573

C--> 28 (B) FILING DATE: 25-Jul-2000

29 (C) CLASSIFICATION:

31 (vii) PRIOR APPLICATION DATA:

32 (A) APPLICATION NUMBER: US/08/446,669

33 (B) FILING DATE: May 25, 1995

36 (viii) ATTORNEY/AGENT INFORMATION:

37 (A) NAME: Neeley, Richard

38 (B) REGISTRATION NUMBER: 30,092

39 (C) REFERENCE/DOCKET NUMBER: UCAL-237/01US

41 (ix) TELECOMMUNICATION INFORMATION:

42 (A) TELEPHONE: 415-843-5000

43 (B) TELEFAX: 415-857-0663

44 (C) TELEX: 380816CooleyPA

45 (2) INFORMATION FOR SEQ ID NO: 1:

47 (i) SEQUENCE CHARACTERISTICS:

49 (A) LENGTH: 2232 base pairs

50 (B) TYPE: nucleic acid

51 (C) STRANDEDNESS: single

52 (D) TOPOLOGY: linear

54 (ii) MOLECULE TYPE: cDNA

56 (iii) HYPOTHETICAL: NO

58 (iv) ANTI-SENSE: NO

ENTERED

RAW SEQUENCE LISTING

DATE: 10/03/2002

PATENT APPLICATION: US/09/625,573

TIME: 14:00:12

Input Set : N:\Crif3\RULE60\09625573.raw

Output Set: N:\CRF4\10032002\I625573.raw

```

60      (ix) FEATURE:
61          (A) NAME/KEY: CDS
62          (B) LOCATION: 40..1161
63      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
64      GGATTGAACA AGGACGCATT TCCCCAGTAC ATCCACAAC ATG CTG TCC ACA TCT      54
65                                     Met Leu Ser Thr Ser
66                                     1      5
67      CGT TCT CGG TTT ATC AGA AAT ACC AAC GAG AGC GGT GAA GAA GTC ACC      102
68      Arg Ser Arg Phe Ile Arg Asn Thr Asn Glu Ser Gly Glu Glu Val Thr
69                                     10      15      20
70      ACC TTT TTT GAT TAT GAT TAC GGT GCT CCC TGT CAT AAA TTT GAC GTG      150
71      Thr Phe Phe Asp Tyr Asp Tyr Gly Ala Pro Cys His Lys Phe Asp Val
72                                     25      30      35
73      AAG CAA ATT GGG GCC CAA CTC CTG CCT CCG CTC TAC TCG CTG GTG TTC      198
74      Lys Gln Ile Gly Ala Gln Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe
75      40      45      50
76      ATC TTT GGT TTT GTG GGC AAC ATG CTG GTC GTC CTC ATC TTA ATA AAC      246
77      Ile Phe Gly Phe Val Gly Asn Met Leu Val Val Leu Ile Leu Ile Asn
78      55      60      65
79      TGC AAA AAG CTG AAG TGC TTG ACT GAC ATT TAC CTG CTC AAC CTG GCC      294
80      Cys Lys Lys Leu Lys Cys Leu Thr Asp Ile Tyr Leu Leu Asn Leu Ala
81      70      75      80      85
82      ATC TCT GAT CTG CTT TTT CTT ATT ACT CTC CCA TTG TGG GCT CAC TCT      342
83      Ile Ser Asp Leu Leu Phe Leu Ile Thr Leu Pro Leu Trp Ala His Ser
84      90      95      100
85      GCT GCA AAT GAG TGG GTC TTT GGG AAT GCA ATG TGC AAA TTA TTC ACA      390
86      Ala Ala Asn Glu Trp Val Phe Gly Asn Ala Met Cys Lys Leu Phe Thr
87      105      110      115
88      GGG CTG TAT CAC ATC GGT TAT TTT GGC GGA ATC TTC TTC ATC ATC CTC      438
89      Gly Leu Tyr His Ile Gly Tyr Phe Gly Gly Ile Phe Phe Ile Ile Leu
90      120      125      130
91      CTG ACA ATC GAT AGA TAC CTG GCT ATT GTC CAT GCT GTG TTT GCT TTA      486
92      Leu Thr Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu
93      135      140      145
94      AAA GCC AGG ACG GTC ACC TTT GGG GTG GTG ACA AGT GTG ATC ACC TGG      534
95      Lys Ala Arg Thr Val Thr Phe Gly Val Val Thr Ser Val Ile Thr Trp
96      150      155      160      165
97      TTG GTG GCT GTG TTT GCT TCT GTC CCA GGA ATC ATC TTT ACT AAA TGC      582
98      Leu Val Ala Val Phe Ala Ser Val Pro Gly Ile Ile Phe Thr Lys Cys
99      170      175      180
100     CAG AAA GAA GAT TCT GTT TAT GTC TGT GGC CCT TAT TTT CCA CGA GGA      630
101     Gln Lys Glu Asp Ser Val Tyr Val Cys Gly Pro Tyr Phe Pro Arg Gly
102     185      190      195
103     TGG AAT AAT TTC CAC ACA ATA ATG AGG AAC ATT TTG GGG CTG GTC CTG      678
104     Trp Asn Asn Phe His Thr Ile Met Arg Asn Ile Leu Gly Leu Val Leu
105     200      205      210
106     CCG CTG CTC ATC ATG GTC ATC TGC TAC TCG GGA ATC CTG AAA ACC CTG      726
107     Pro Leu Leu Ile Met Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu
108     215      220      225

```

RAW SEQUENCE LISTING

DATE: 10/03/2002

PATENT APPLICATION: US/09/625,573

TIME: 14:00:12

Input Set : N:\Crif3\RULE60\09625573.raw

Output Set: N:\CRF4\10032002\I625573.raw

```

128 CTT CGG TGT CGA AAC GAG AAG AAG AGG CAT AGG GCA GTG AGA GTC ATC      774
129 Leu Arg Cys Arg Asn Glu Lys Lys Arg His Arg Ala Val Arg Val Ile
130 230      235      240      245
132 TTC ACC ATC ATG ATT GTT TAC TTT CTC TTC TGG ACT CCC TAT AAC ATT      822
133 Phe Thr Ile Met Ile Val Tyr Phe Leu Phe Trp Thr Pro Tyr Asn Ile
134      250      255      260
136 GTC ATT CTC CTG AAC ACC TTC CAG GAA TTC TTC GGC CTG AGT AAC TGT      870
137 Val Ile Leu Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu Ser Asn Cys
138      265      270      275
140 GAA AGC ACC AGT CAA CTG GAC CAA GCC ACG CAG GTG ACA GAG ACT CTT      918
141 Glu Ser Thr Ser Gln Leu Asp Gln Ala Thr Gln Val Thr Glu Thr Leu
142      280      285      290
144 GGG ATG ACT CAC TGC TGC ATC AAT CCC ATC ATC TAT GCC TTC GTT GGG      966
145 Gly Met Thr His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe Val Gly
146      295      300      305
148 GAG AAG TTC AGA AGC CTT TTT CAC ATA GCT CTT GGC TGT AGG ATT GCC      1014
149 Glu Lys Phe Arg Ser Leu Phe His Ile Ala Leu Gly Cys Arg Ile Ala
150 310      315      320      325
152 CCA CTC CAA AAA CCA CTG TGT GGA GGT CCA GGA GTG AGA CCA GGA AAG      1062
153 Pro Leu Gln Lys Pro Val Cys Gly Gly Pro Gly Val Arg Pro Gly Lys
154      330      335      340
156 AAT GTG AAA GTG ACT ACA CAA GGA CTC CTC GAT GGT CGT GGA AAA GGA      1110
157 Asn Val Lys Val Thr Thr Gln Gly Leu Leu Asp Gly Arg Gly Lys Gly
158      345      350      355
160 AAG TCA ATT GGC AGA GCC CCT GAA GCC AGT CTT CAG GAC AAA GAA GGA      1158
161 Lys Ser Ile Gly Arg Ala Pro Glu Ala Ser Leu Gln Asp Lys Glu Gly
162      360      365      370
164 GCC TAGAGACAGA AATGACAGAT CTCTGCTTTG GAAATCACAC GTCTGGCTTC      1211
165 Ala
167 ACAGATGTGT GATTACACAGT GTGAATCTTG GTGTCTACGT TACCAGGCAG GAAGGCTGAG      1271
169 AGGAGAGAGA CTCCAGCTGG GTTGGAAC AGTATTTTCC AAACCTACCTT CCAGTTCCCTC      1331
171 ATTTTTGAAT ACAGGCATAG AGTTCAGACT TTTTAAAT AGTAAAAATA AAATTAAAGC      1391
173 TGAAACTGC AACTTGTAAG TGTGGTAAAG AGTTAGTTTG AGTTGCTATC ATGTCAAACG      1451
175 TGAAATGCT GTATTAGTCA CAGAGATAAT TCTAGCTTTG AGCTTAAGAA TTTTGAGCAG      1511
177 GTGGTATGTT TGGGAGACTG CTGAGTCAAC CCAATAGTTG TTGATTGGCA GGAGTTGGAA      1571
179 GTGTGTGATC TGTGGGCACA TTAGCCTATG TGCATGCAGC ATCTAAGTAA TGATGTCGTT      1631
181 TGAATCACAG TATACGCTCC ATCGCTGTCA TCTCAGCTGG ATCTCCATTC TCTCAGGCTT      1691
183 GCTGCCAAAA GCCTTTTGTG TTTTGTTTTG TATCATTATG AAGTCATGCG TTTAATCACA      1751
185 TTCGAGTGTT TCAGTGCTTC GCAGATGTCC TTGATGCTCA TATTGTTCCC TAATTTGCCA      1811
187 GTGGGAATC CTAAATCAAA TTGGCTTCTA ATCAAAGCTT TTAAACCCTA TTGGTAAAGA      1871
189 ATGGAAGGTG GAGAAGCTCC CTGAAGTAAG CAAAGACTTT CCTCTTAGTC GAGCCAAGTT      1931
191 AAGAATGTTT TTATGTTGCC CAGTGTGTTT CTGATCTGAT GCAAGCAAGA AACACTGGGC      1991
193 TTCTAGAACC AGGCAACTTG GGAAGTAGAC TCCAAGCTG GACTATGGCT CTACTTTCAG      2051
195 GCCACATGGC TAAAGAAGGT TTCAGAAAGA AGTGGGGACA GAGCAGAACT TTCACCTTCA      2111
197 TATATTTGTA TGATCCTAAT GAATGCATAA AATGTTAAGT TGATGGTGAT GAAATGTAAA      2171
199 TACTGTTTTT AACAACATAT ATTTGGAAAA TAAATCAATG CTATAACTAT GTTGATAAAA      2231
201 G      2232
204 (2) INFORMATION FOR SEQ ID NO: 2:
206 (i) SEQUENCE CHARACTERISTICS:

```

RAW SEQUENCE LISTING

DATE: 10/03/2002

PATENT APPLICATION: US/09/625,573

TIME: 14:00:12

Input Set : N:\Crif3\RULE60\09625573.raw

Output Set: N:\CRF4\10032002\I625573.raw

207 (A) LENGTH: 374 amino acids
 208 (B) TYPE: amino acid
 209 (D) TOPOLOGY: linear
 211 (ii) MOLECULE TYPE: protein
 213 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 216 Met Leu Ser Thr Ser Arg Ser Arg Phe Ile Arg Asn Thr Asn Glu Ser
 217 1 5 10 15
 219 Gly Glu Glu Val Thr Thr Phe Phe Asp Tyr Asp Tyr Gly Ala Pro Cys
 220 20 25 30
 222 His Lys Phe Asp Val Lys Gln Ile Gly Ala Gln Leu Leu Pro Pro Leu
 223 35 40 45
 225 Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn Met Leu Val Val
 226 50 55 60
 228 Leu Ile Leu Ile Asn Cys Lys Lys Leu Lys Cys Leu Thr Asp Ile Tyr
 229 65 70 75 80
 231 Leu Leu Asn Leu Ala Ile Ser Asp Leu Leu Phe Leu Ile Thr Leu Pro
 232 85 90 95
 234 Leu Trp Ala His Ser Ala Ala Asn Glu Trp Val Phe Gly Asn Ala Met
 235 100 105 110
 237 Cys Lys Leu Phe Thr Gly Leu Tyr His Ile Gly Tyr Phe Gly Gly Ile
 238 115 120 125
 240 Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu Ala Ile Val His
 241 130 135 140
 243 Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe Gly Val Val Thr
 244 145 150 155 160
 246 Ser Val Ile Thr Trp Leu Val Ala Val Phe Ala Ser Val Pro Gly Ile
 247 165 170 175
 249 Ile Phe Thr Lys Cys Gln Lys Glu Asp Ser Val Tyr Val Cys Gly Pro
 250 180 185 190
 252 Tyr Phe Pro Arg Gly Trp Asn Asn Phe His Thr Ile Met Arg Asn Ile
 253 195 200 205
 255 Leu Gly Leu Val Leu Pro Leu Leu Ile Met Val Ile Cys Tyr Ser Gly
 256 210 215 220
 258 Ile Leu Lys Thr Leu Leu Arg Cys Arg Asn Glu Lys Lys Arg His Arg
 259 225 230 235 240
 261 Ala Val Arg Val Ile Phe Thr Ile Met Ile Val Tyr Phe Leu Phe Trp
 262 245 250 255
 264 Thr Pro Tyr Asn Ile Val Ile Leu Leu Asn Thr Phe Gln Glu Phe Phe
 265 260 265 270
 267 Gly Leu Ser Asn Cys Glu Ser Thr Ser Gln Leu Asp Gln Ala Thr Gln
 268 275 280 285
 270 Val Thr Glu Thr Leu Gly Met Thr His Cys Cys Ile Asn Pro Ile Ile
 271 290 295 300
 273 Tyr Ala Phe Val Gly Glu Lys Phe Arg Ser Leu Phe His Ile Ala Leu
 274 305 310 315 320
 276 Gly Cys Arg Ile Ala Pro Leu Gln Lys Pro Val Cys Gly Gly Pro Gly
 277 325 330 335
 279 Val Arg Pro Gly Lys Asn Val Lys Val Thr Thr Gln Gly Leu Leu Asp
 280 340 345 350

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/625,573

DATE: 10/03/2002

TIME: 14:00:12

Input Set : N:\Crf3\RULE60\09625573.raw

Output Set: N:\CRF4\10032002\I625573.raw

```

282 Gly Arg Gly Lys Gly Lys Ser Ile Gly Arg Ala Pro Glu Ala Ser Leu
283           355                      360                      365
285 Gln Asp Lys Glu Gly Ala
286           370
289 (2) INFORMATION FOR SEQ ID NO: 3:
291     (i) SEQUENCE CHARACTERISTICS:
292         (A) LENGTH: 1979 base pairs
293         (B) TYPE: nucleic acid
294         (C) STRANDEDNESS: single
295         (D) TOPOLOGY: linear
297     (ii) MOLECULE TYPE: cDNA
299     (iii) HYPOTHETICAL: NO
301     (iv) ANTI-SENSE: NO
303     (ix) FEATURE:
304         (A) NAME/KEY: CDS
305         (B) LOCATION: 81..1160
307     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
310 CAGGACTGCC TGAGACAAGC CACAAGCTGA ACAGAGAAAG TGGATTGAAC AAGGACGCAT      60
312 TTCCCCAGTA CATCCACAAC ATG CTG TCC ACA TCT CGT TCT CGG TTT ATC      110
313           Met Leu Ser Thr Ser Arg Ser Arg Phe Ile
314           1                      5                      10
316 AGA AAT ACC AAC GAG AGC GGT GAA GAA GTC ACC ACC TTT TTT GAT TAT      158
317 Arg Asn Thr Asn Glu Ser Gly Glu Glu Val Thr Thr Phe Phe Asp Tyr
318           15                      20                      25
320 GAT TAC GGT GCT CCC TGT CAT AAA TTT GAC GTG AAG CAA ATT GGG GCC      206
321 Asp Tyr Gly Ala Pro Cys His Lys Phe Asp Val Lys Gln Ile Gly Ala
322           30                      35                      40
324 CAA CTC CTG CCT CCG CTC TAC TCG CTG GTG TTC ATC TTT GGT TTT GTG      254
325 Gln Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val
326           45                      50                      55
328 GGC AAC ATG CTG GTC GTC CTC ATC TTA ATA AAC TGC AAA AAG CTG AAG      302
329 Gly Asn Met Leu Val Val Leu Ile Leu Ile Asn Cys Lys Lys Leu Lys
330           60                      65                      70
332 TGC TTG ACT GAC ATT TAC CTG CTC AAC CTG GCC ATC TCT GAT CTG CTT      350
333 Cys Leu Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Leu
334           75                      80                      85                      90
336 TTT CTT ATT ACT CTC CCA TTG TGG GCT CAC TCT GCT GCA AAT GAG TGG      398
337 Phe Leu Ile Thr Leu Pro Leu Trp Ala His Ser Ala Ala Asn Glu Trp
338           95                      100                      105
340 GTC TTT GGG AAT GCA ATG TGC AAA TTA TTC ACA GGG CTG TAT CAC ATC      446
341 Val Phe Gly Asn Ala Met Cys Lys Leu Phe Thr Gly Leu Tyr His Ile
342           110                      115                      120
344 GGT TAT TTT GGC GGA ATC TTC TTC ATC ATC CTC CTG ACA ATC GAT AGA      494
345 Gly Tyr Phe Gly Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg
346           125                      130                      135
348 TAC CTG GCT ATT GTC CAT GCT GTG TTT GCT TTA AAA GCC AGG ACG GTC      542
349 Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val
350           140                      145                      150
352 ACC TTT GGG GTG GTG ACA AGT GTG ATC ACC TGG TTG GTG GCT GTG TTT      590

```

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/625,573

DATE: 10/03/2002

TIME: 14:00:13

Input Set : N:\Crf3\RULE60\09625573.raw

Output Set: N:\CRF4\10032002\I625573.raw

L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]

L:856 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=9

L:874 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=10